How to Install and Use the Fresh Model in R

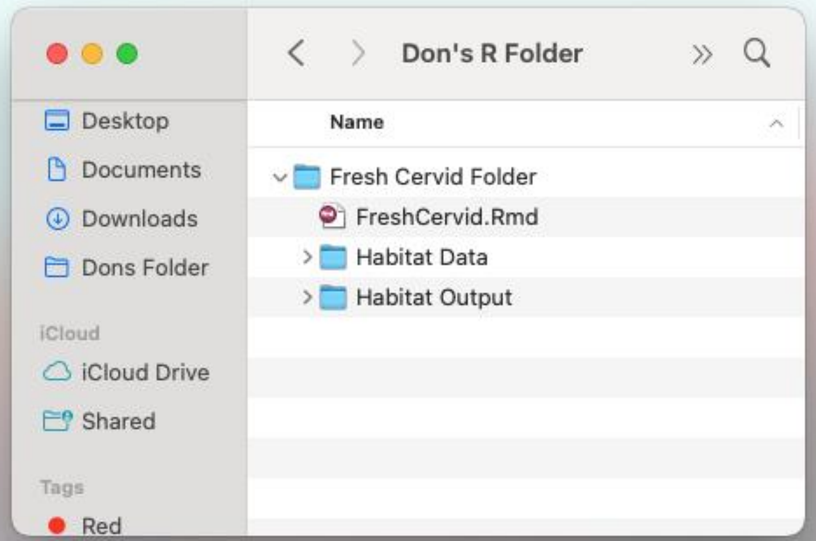
For those unfamiliar with R or R Studio (a more user-friendly version of R) -

Start Here 

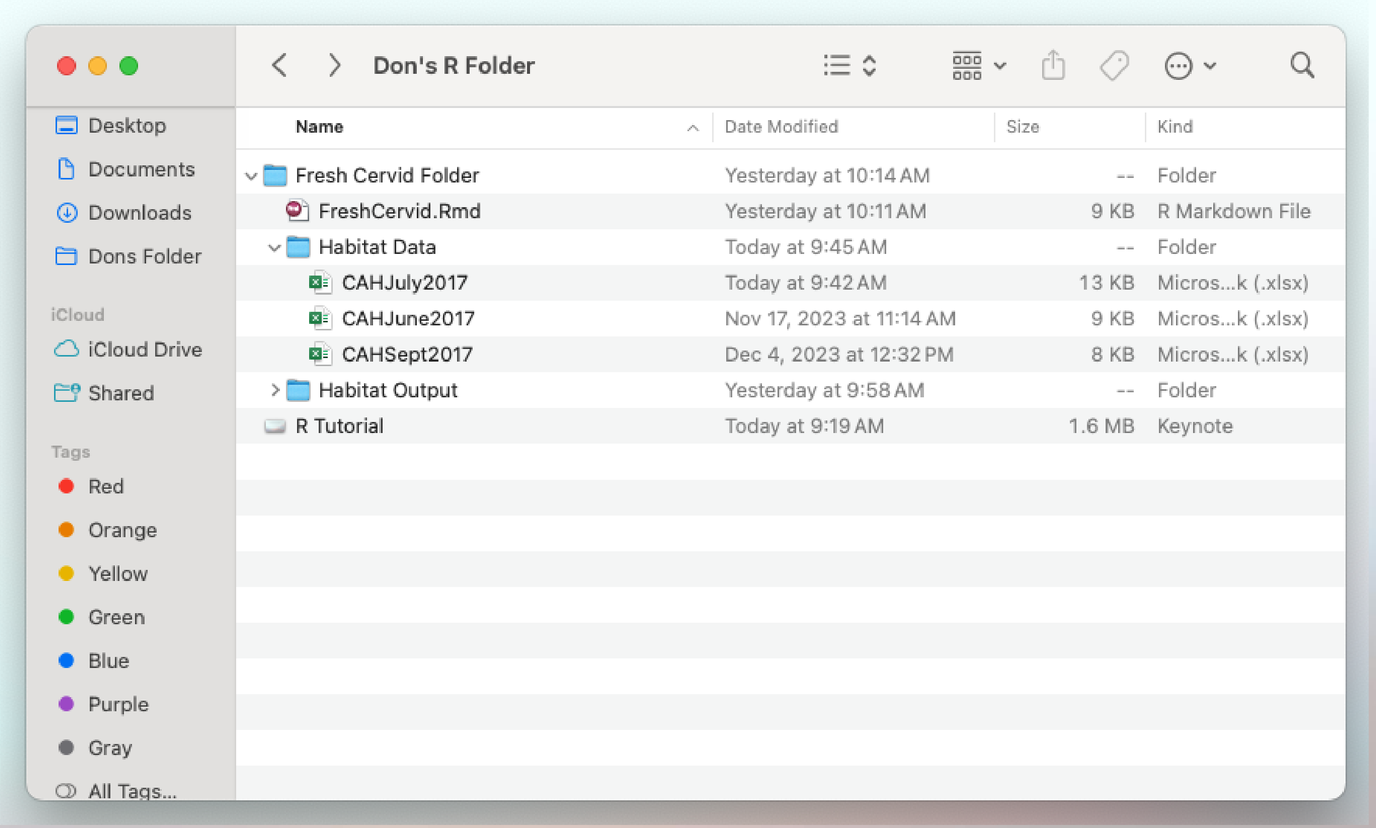
1. Assuming you have installed R Studio on your computer, create a Folder for your work and copy the “FreshCervid.R” script into this Folder.

2. Within this folder, create two new folders, one of which will contain the excel files (.xlsx files) that describe the habitat (or habitats) that you wish to examine. The other folder will contain the outputs of the FRESH model.

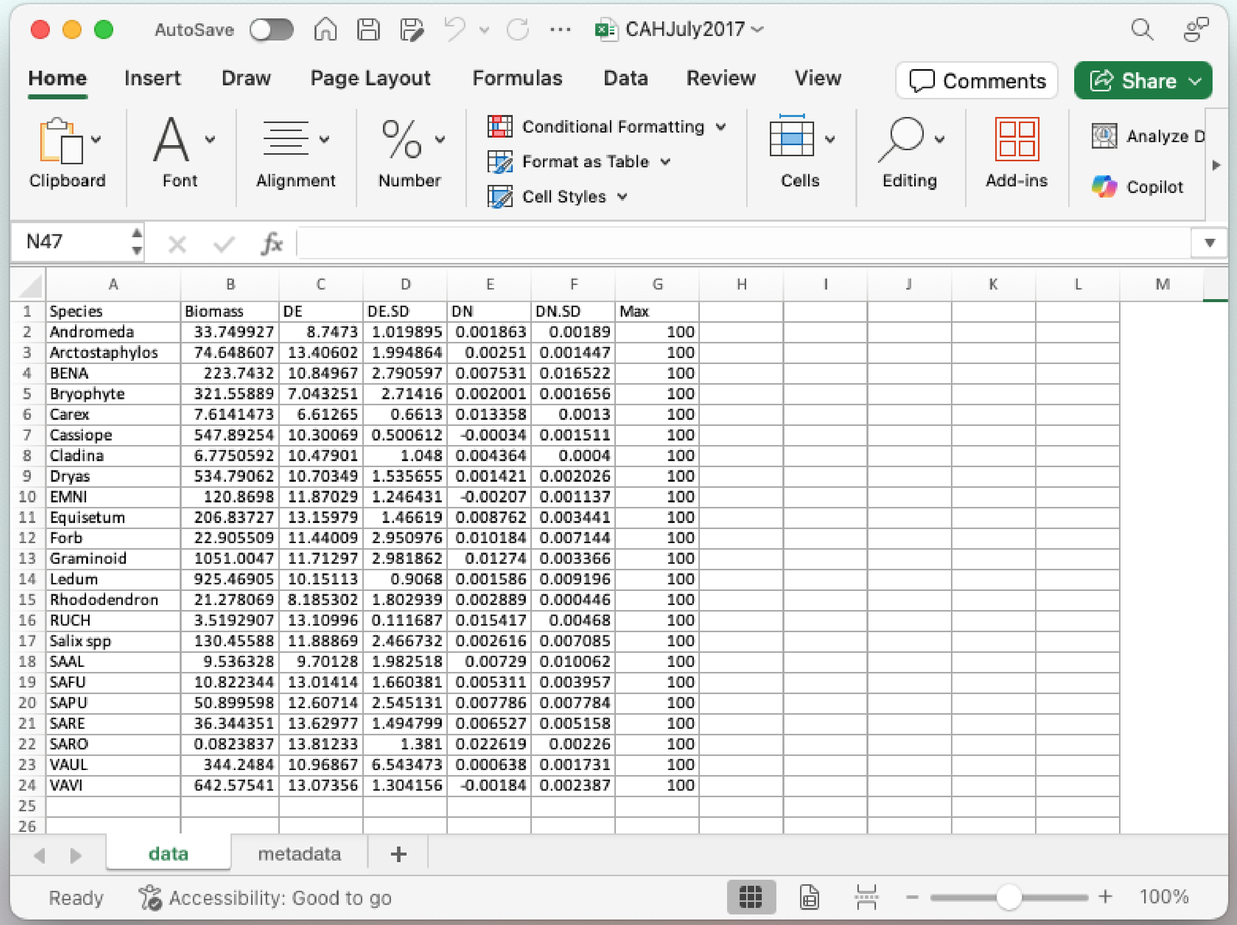
Here is an example of what this might look like:



3. Next, create the excel data files that you wish to examine with the FRESHCervid model. For this example, I wish to analyze habitat and nutritional data collected in a recent study of the Central Arctic Caribou herd. In the Habitat folder, I have placed three data files of habitat and nutrition data collected in June, July, and September from this study area. Here is what my file structure now looks like:



4. Each Excel file in the Habitat Data folder contains two sheets: a “data” sheet, and a “metadata” sheet. The data sheet contains the mean nutritional characteristics and biomass densities of the individual plants available to the herbivore in the habitat, along with the variance for each of the parameters. Here is an example of one of these CAH data sheet:



	A	B	C	D	E	F	G	H	I	J	K	L	M
1	Species	Biomass	DE	DE.SD	DN	DN.SD	Max						
2	Andromeda	33.749927	8.7473	1.019895	0.001863	0.00189	100						
3	Arctostaphylos	74.648607	13.40602	1.994864	0.00251	0.001447	100						
4	BENA	223.7432	10.84967	2.790597	0.007531	0.016522	100						
5	Bryophyte	321.55889	7.043251	2.71416	0.002001	0.001656	100						
6	Carex	7.6141473	6.61265	0.6613	0.013358	0.0013	100						
7	Cassiope	547.89254	10.30069	0.500612	-0.00034	0.001511	100						
8	Cladina	6.7750592	10.47901	1.048	0.004364	0.0004	100						
9	Dryas	534.79062	10.70349	1.535655	0.001421	0.002026	100						
10	EMNI	120.8698	11.87029	1.246431	-0.00207	0.001137	100						
11	Equisetum	206.83727	13.15979	1.46619	0.008762	0.003441	100						
12	Forb	22.905509	11.44009	2.950976	0.010184	0.007144	100						
13	Graminoid	1051.0047	11.71297	2.981862	0.01274	0.003366	100						
14	Ledum	925.46905	10.15113	0.9068	0.001586	0.009196	100						
15	Rhododendron	21.278069	8.185302	1.802939	0.002889	0.000446	100						
16	RUCH	3.5192907	13.10996	0.111687	0.015417	0.00468	100						
17	Salix spp	130.45588	11.88869	2.466732	0.002616	0.007085	100						
18	SAAL	9.536328	9.70128	1.982518	0.00729	0.010062	100						
19	SAFU	10.822344	13.01414	1.660381	0.005311	0.003957	100						
20	SAPU	50.899598	12.60714	2.545131	0.007786	0.007784	100						
21	SARE	36.344351	13.62977	1.494799	0.006527	0.005158	100						
22	SARO	0.0823837	13.81233	1.381	0.022619	0.00226	100						
23	VAUL	344.2484	10.96867	6.543473	0.000638	0.001731	100						
24	VAVI	642.57541	13.07356	1.304156	-0.00184	0.002387	100						
25													
26													

Note 1: The units of each of the parameters are not specified in the label for the columns. I try to keep the label for each column as simple as possible in R data files, simplifying R programming and data labeling issues down the line.

Note 2: Regarding data units in this example: you can use whatever units you are familiar with in this program (e.g., DE, or “digestible energy” can be in kcal/g, or kj/g - which are the units in this example), but you must be careful to keep these consistent throughout. The units of DN in this example (and likewise DN.SD) is in g DN per g of DM (i.e., Dry Matter). It could also be expressed as g/kg DM, if desired….just keep the units consistent throughout the process.

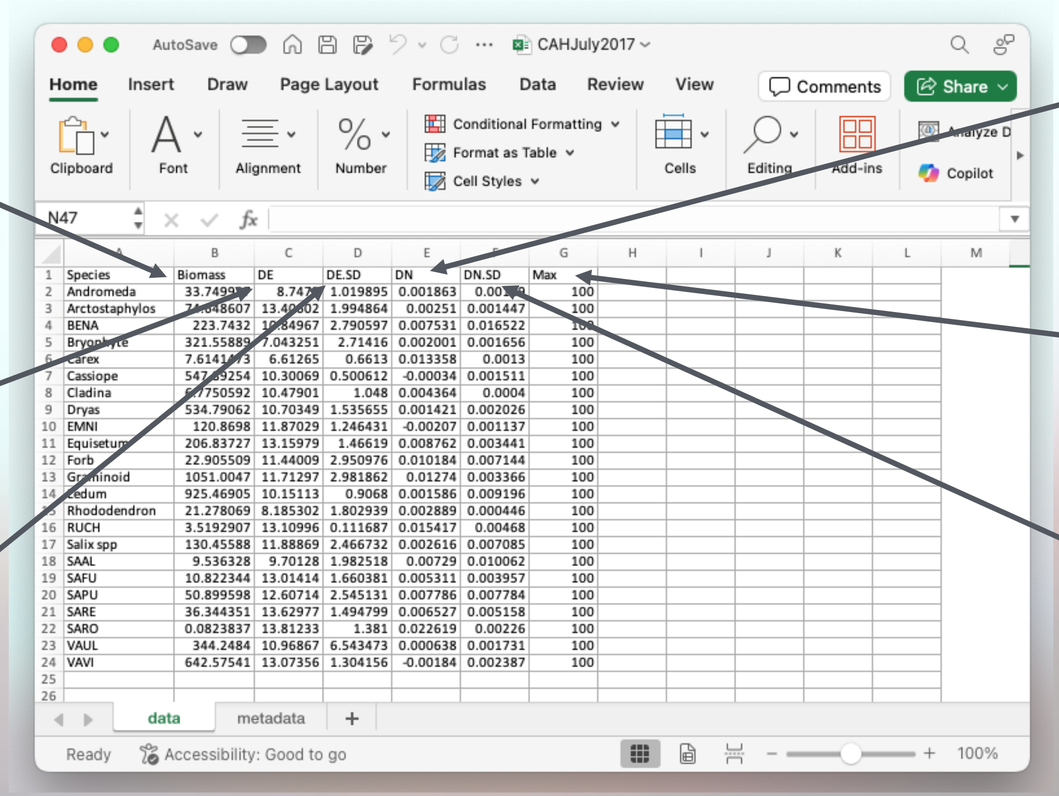
More about Units of Measurement

Generally, data in spreadsheets should contain precise and standard nomenclature, including units of measurement, but R has specific and idiosyncratic ways of formatting column data names, and thus it is often better to use simple 1 word titles for these identifiers, to keep things simple. In the case below, I do this, and I point out here what these column names mean, and what their units are. Another way to handle this is with an additional sheet in your data file that covers these details without complicating your column names.

Biomass Density (kg/ha)

Digestible Energy (kJ/g Dry Matter)

Standard Deviation of Digestible Energy (kJ/g Dry Matter)



	Species	Biomass	DE	DE.SD	DN	DN.SD	Max
2	Andromeda	33.74993	8.747	1.019895	0.001863	0.00179	100
3	Arctostaphylos	74.048607	13.40802	1.994864	0.00251	0.001447	100
4	BENA	223.7432	10.84967	2.790597	0.007531	0.016522	100
5	Bryophyte	321.55889	7.043251	2.71416	0.002001	0.001656	100
6	Carex	7.6141093	6.61265	0.6613	0.013358	0.0013	100
7	Cassiope	547.89254	10.30069	0.500612	-0.00034	0.001511	100
8	Cladina	67.750592	10.47901	1.048	0.004364	0.0004	100
9	Dryas	534.79062	10.70349	1.535655	0.001421	0.002026	100
10	EMNI	120.8698	11.87029	1.246431	-0.00207	0.001137	100
11	Equisetum	206.83727	13.15979	1.46619	0.008762	0.003441	100
12	Forb	22.905509	11.44009	2.950976	0.010184	0.007144	100
13	Graminoid	1051.0047	11.71297	2.981862	0.01274	0.003366	100
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18	SAAL	9.536328	9.70128	1.982518	0.00729	0.010062	100
19	SAFU	10.822344	13.01414	1.660381	0.005311	0.003957	100
20	SAPU	50.899598	12.60714	2.545131	0.007786	0.007784	100
21	SARE	36.344351	13.62977	1.494799	0.006527	0.005158	100
22	SARO	0.0823837	13.81233	1.381	0.022619	0.00226	100
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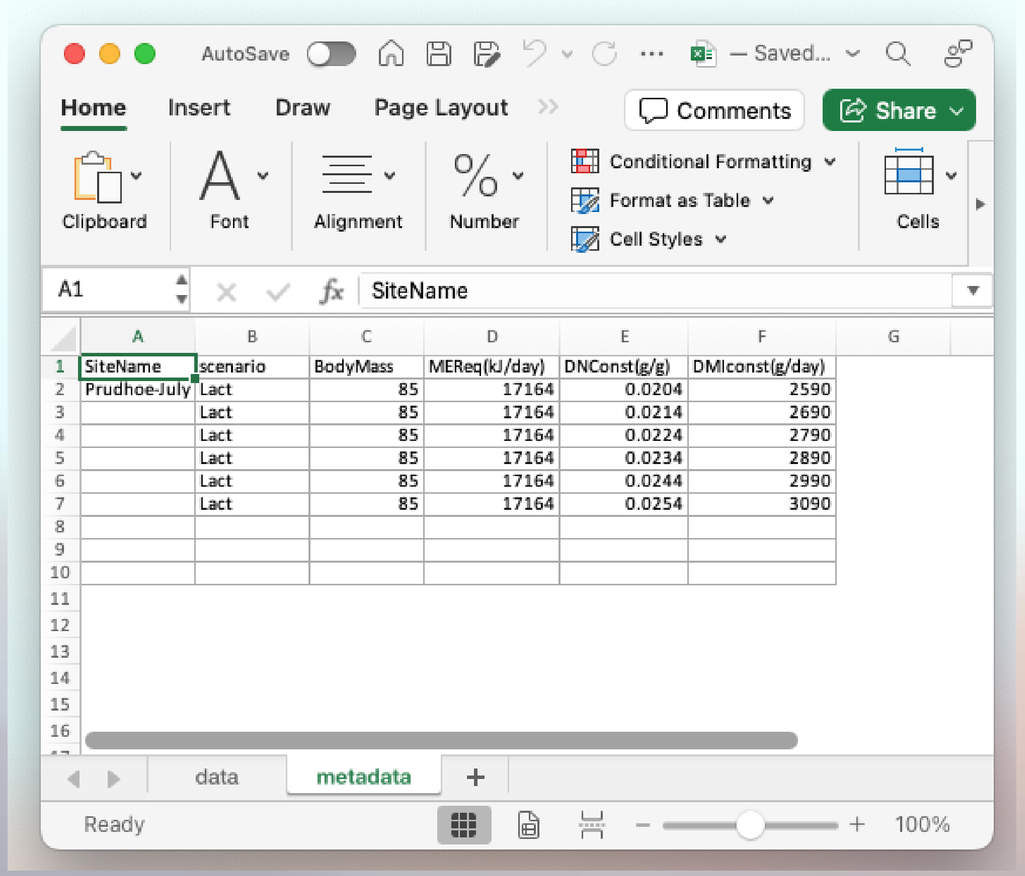
24	VAVI	642.57541	13.07356	1.304156	-0.00184	0.002387	100

Digestible Nitrogen (g/g Dry Matter)

Maximum proportion of the biomass that is available that can be included in the diet (% of Biomass Density)

Standard Deviation of Digestible Nitrogen (g N/g Dry Matter)

5. The second data sheet in each data file, the “metadata”, specifies the characteristics of the analysis (e.g. in this case, the Site Name and the scenario we are simulating (a lactating female), and the conditions (i.e., body weight of animal to be simulated) and constraints of the run (energy requirement to be met, digestible N (i.e., crude protein) that must be met, and the maximum daily dry matter intake that an animal can consume.



	A	B	C	D	E	F	G
1	SiteName	scenario	BodyMass	MEReq(kJ/day)	DNConst(g/g)	DMIconst(g/day)	
2	Prudhoe-July	Lact	85	17164	0.0204	2590	
3		Lact	85	17164	0.0214	2690	
4		Lact	85	17164	0.0224	2790	
5		Lact	85	17164	0.0234	2890	
6		Lact	85	17164	0.0244	2990	
7		Lact	85	17164	0.0254	3090	
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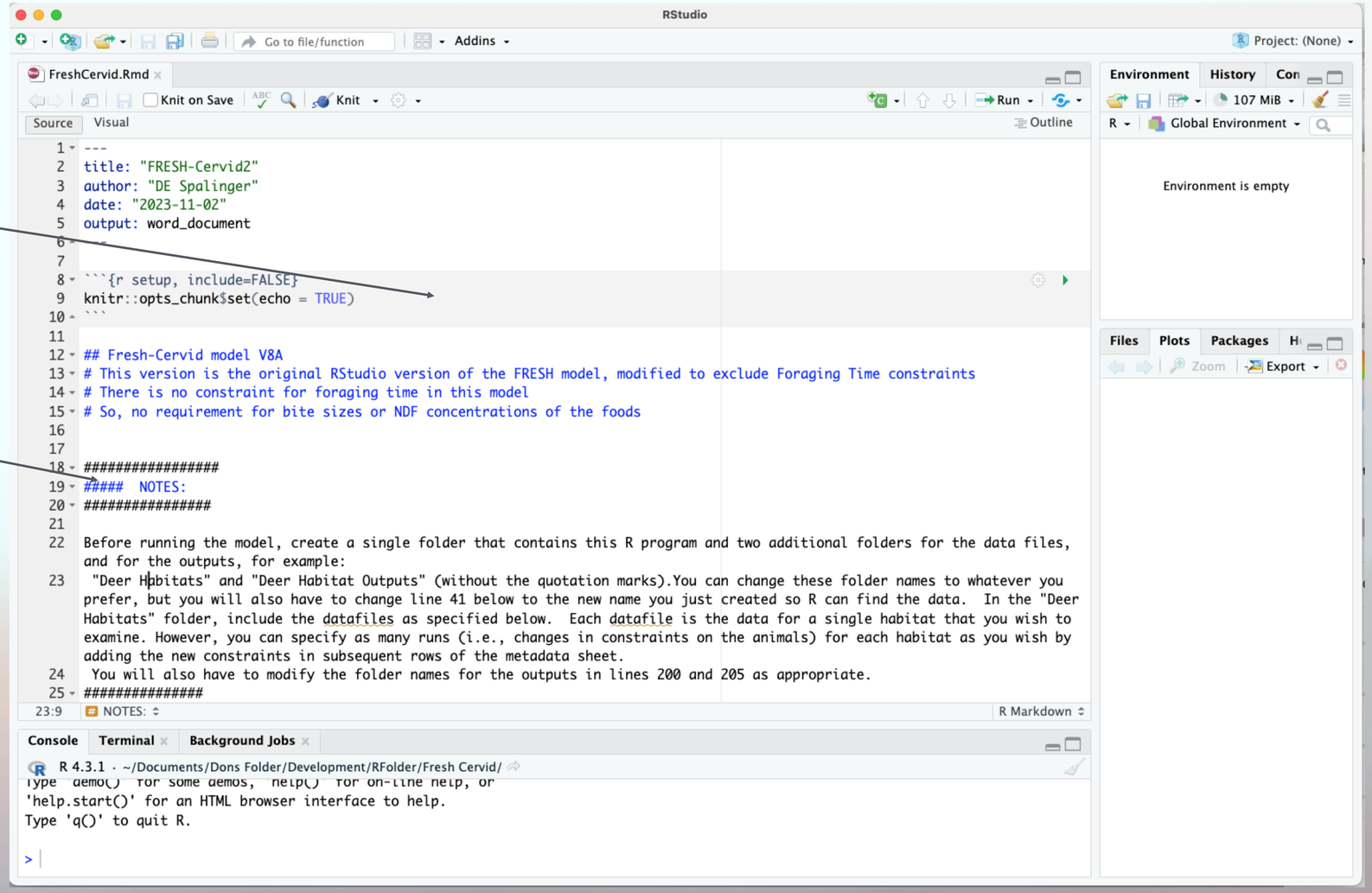
Note: here we have 6 different simulations listed, in which we modify only the daily dry matter intake and the minimum DN concentration of the diet that must be consumed. Hence, it illustrates that you can run more than one simulation at a time. In this case, the animals can eat more per day, but the diet must contain a slightly higher minimum N concentration (both of which are reasonable for a lactating cow caribou).

Once you have completed the setup as described, it is time to run the model:

Open the R Studio version of the Fresh Cervid Model by double clicking it. It should look like this:

Note the shaded box in the script with the little green arrow in the top right of the box. These are code snippets that you will run in sequence. This first snippet just sets up the R Studio run.

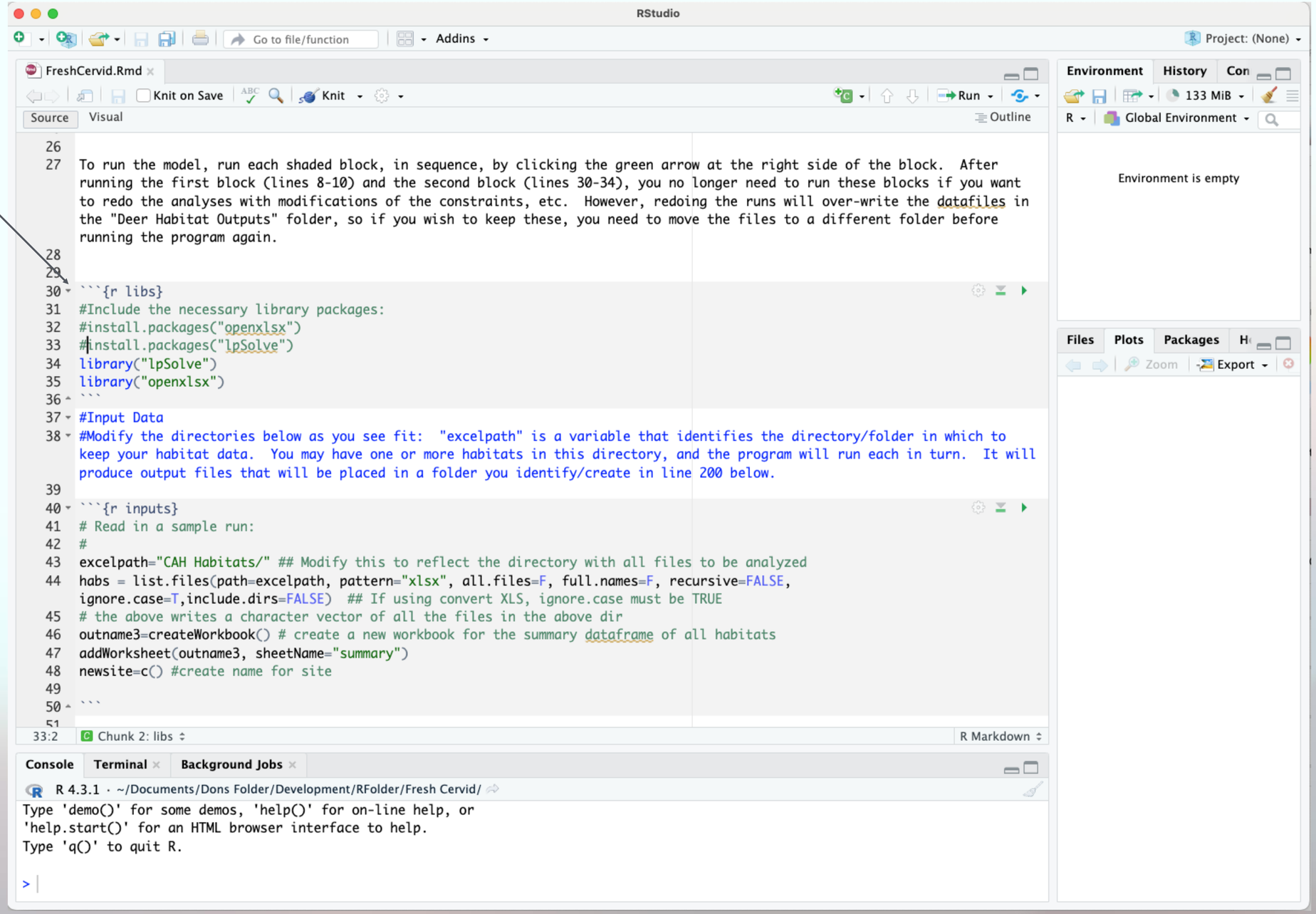
Note the “Notes” instructions. Unfortunately, I did not waste a lot of time making a sophisticated, interactive program…I’m a biologist, remember! So, there are several places that you will need to modify the code to suit your specific needs. So watch out for these “Notes”



Here is the next snippet of code. This adds two external libraries that are necessary for the model. The library “lpSolve” is the code for the solution of the linear programming optimization, and “openxlsx” allows R to read and write excel files for you.

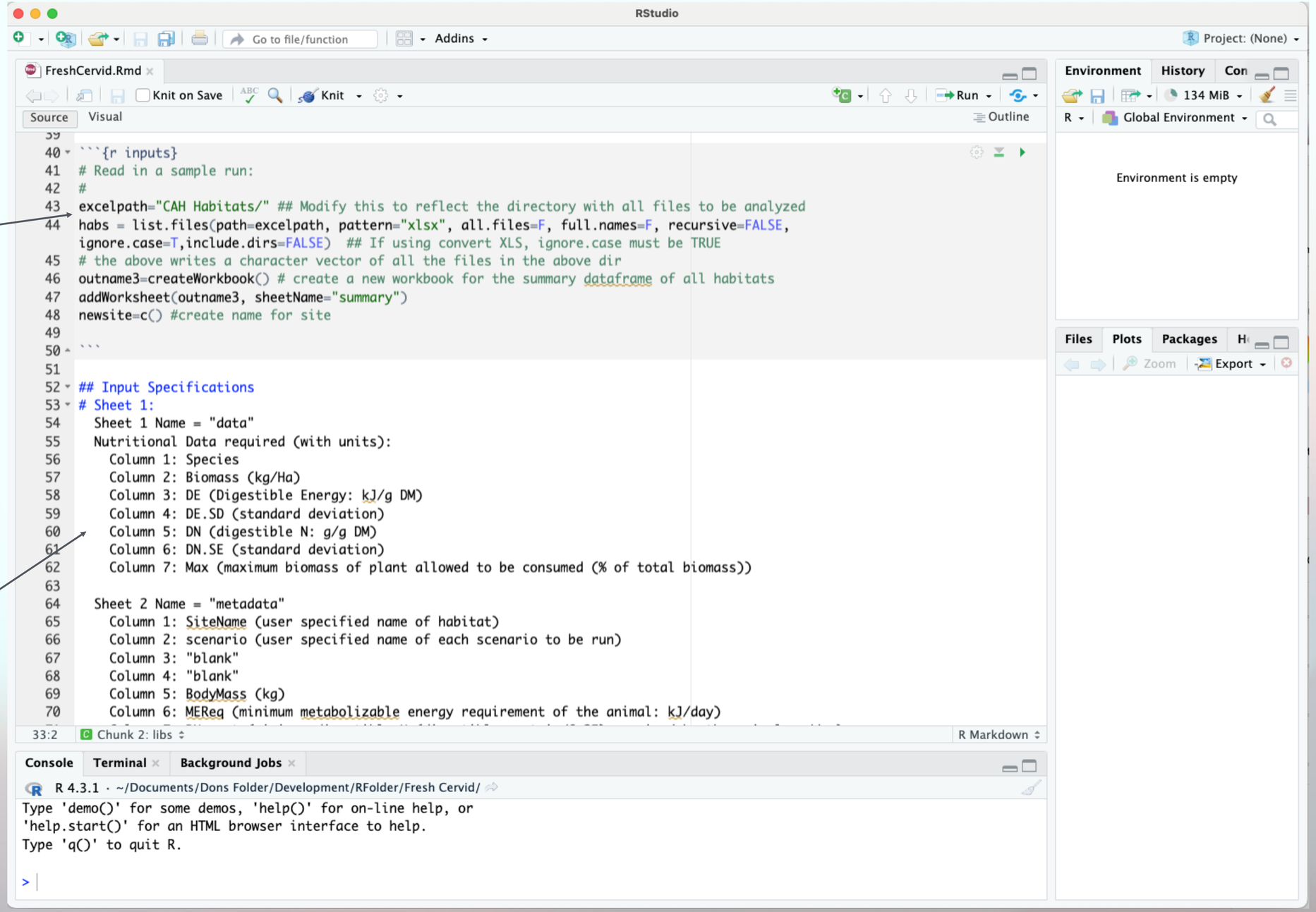
Once this chunk of code is run, you do not need to rerun until the next time you open the FreshCervid model.

Notice that the first two lines of this code are “commented out” (signified by the # sign at the beginning of the line), meaning R ignores anything with a # before it. In this case, these two lines of code do not need to be run because R already has these two programs in its database. For those running this program for the first time, you will need to delete the # sign, and let R go get this code so in the future it can load it from its memory on your machine. Don’t forget to add back the # for each line after running them for the first time.

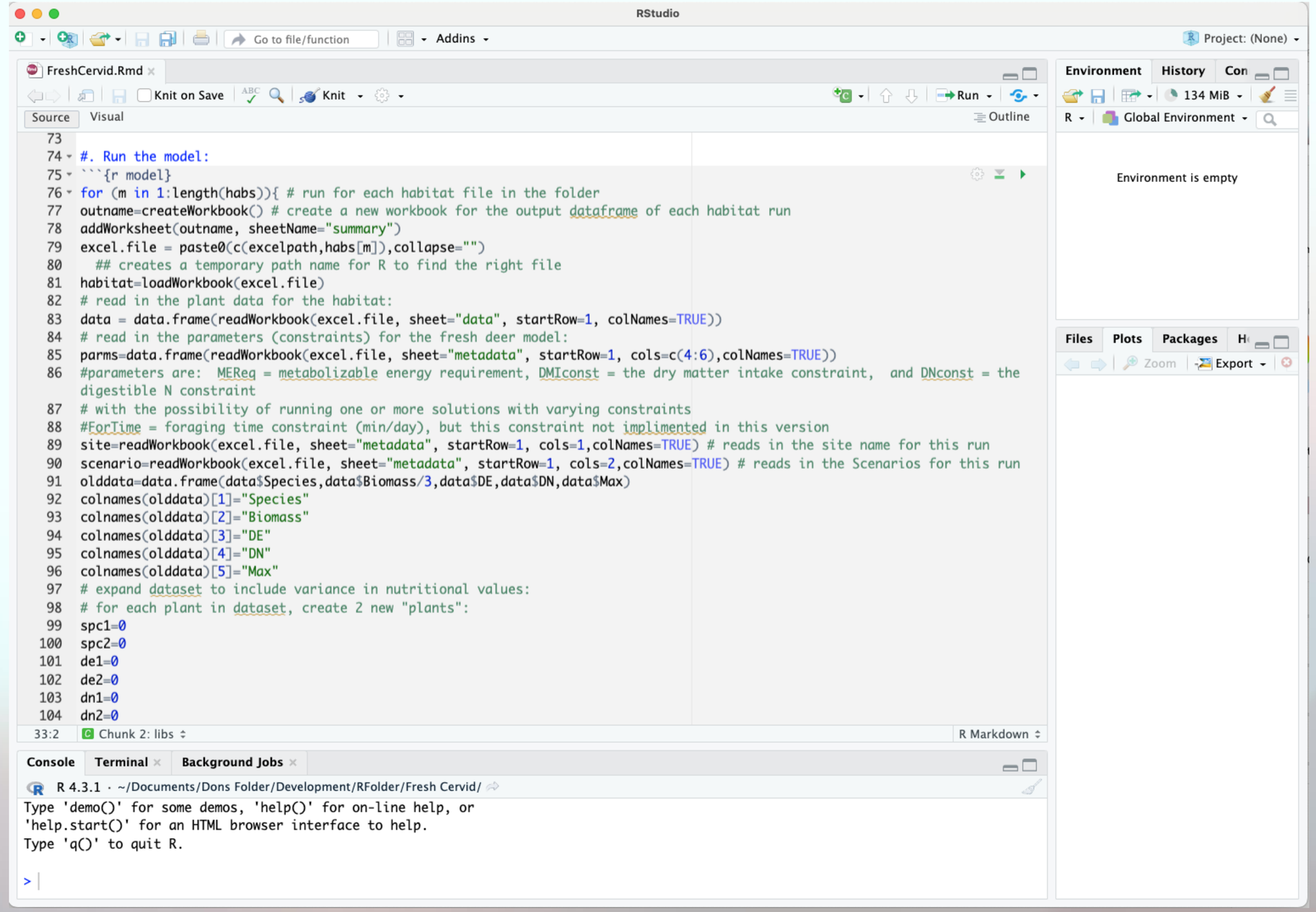


The 3rd chunk of code, shown here, also needs your attention. If you have set up your file structure as specified in this Tutorial, you will need to tell R what the file name for the data files actually is (line 43). Simply change the “CAH Habitats/“ to your new file name (with the / included). This tells R where to go to get your data.

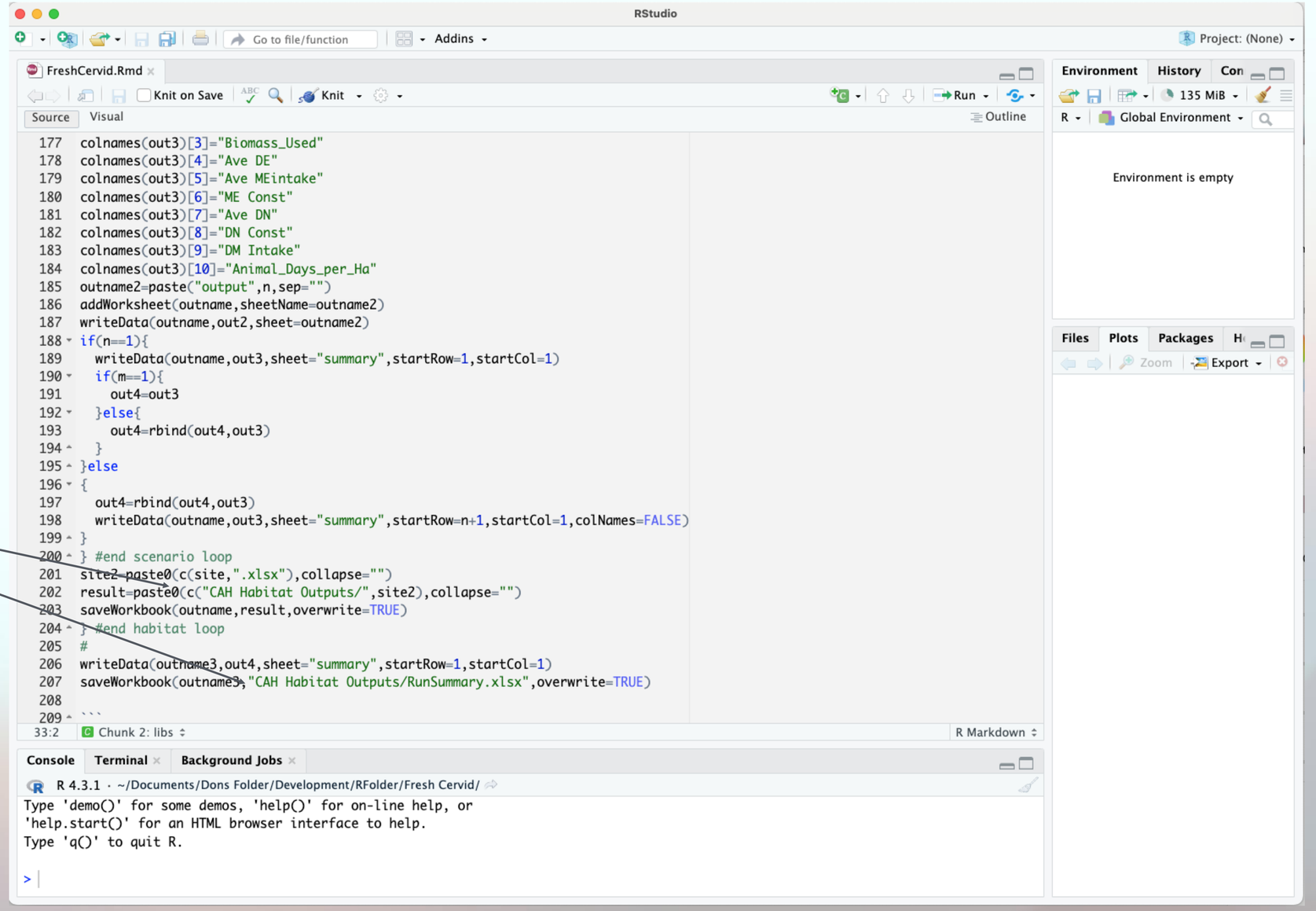
This chunk of text (white background) is where I specify all of the units and names of my variables/data. You can change this as appropriate for your runs, if necessary (R ignores the white background text - its just for humans)



Its just about time to run the Model! The only thing left is to first change the name of the folder in which you want R to file the outputs. This code is in lines 202 and 207 - change the name of the file folder to match that in your directory. Once done, press the little green arrow in the upper right, and you should soon get the output on your computer.



Change the text in these two lines as appropriate for your folders.



Output from your model run

Assuming the model ran successfully, open the Folder “Habitat Output” to examine the results, and you should see 4 new excel files, one for each month, and one summary file of the run.

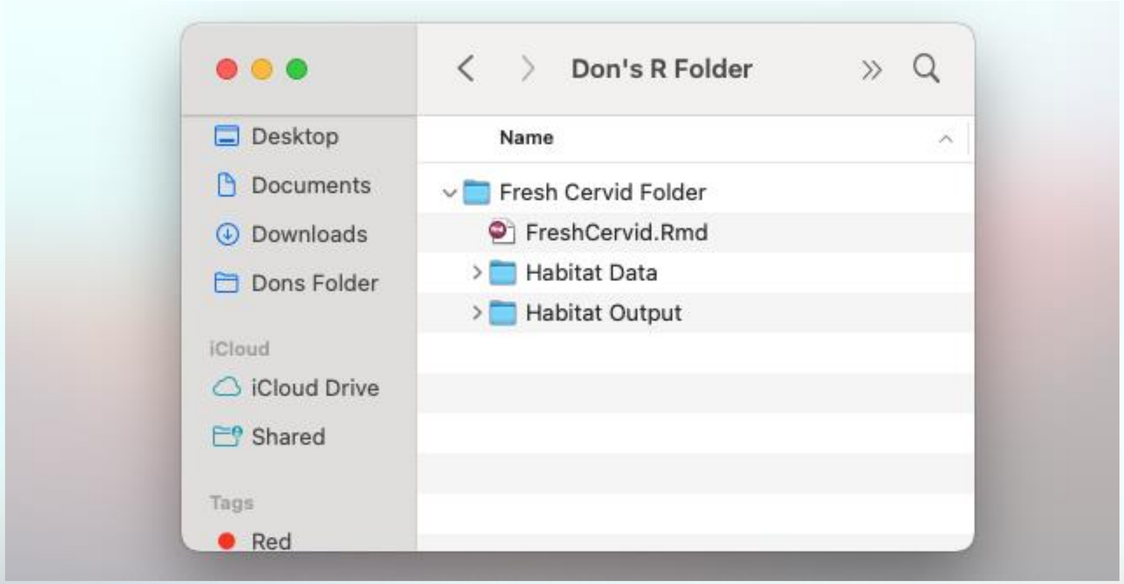
Installing and working with R Studio on your computer

1. Create space for your R work
2. Install the R Studio program
3. Organizing your R scripts, data, and outputs from your modeling sessions

1. Create space for your R work

R scripts (i.e., programs) run from wherever you R script is saved on your computer, and it needs to be told where to go to find any files that are needed to run that script - and it starts looking from wherever your script is stored. If you don't tell it exactly where the data is, it will give up immediately, and throw an error. Hence, I create a folder on my computer where I do all of my R programming (I.e., I keep the actual R program in this folder, and this I establish as my root directory (or folder) for this work. To keep things orderly, I then create additional folders within that folder for data, output, and anything else I need to keep track of for that R program (ie., directions how to use the program, notes on its outputs, etc). If R needs to use these files, then I simply tell R that they are in whatever folder I store this information, and it goes and looks for them when it needs to.

1. **Create space for your work:** To emphasize all of this: you can organize your work however you please, but the main thing you must do is make sure your R script and the data files associated with your Fresh modeling exercise are in the same folder. The data files for the run or runs can be in separate folders under the main folder containing your R script, but you will have to direct R to these subfolders in each run.



For example: my R program, FreshCervid.Rmd, is in a folder called Fresh Cervid Folder. The data and the outputs from the FreshCervid model are included as sub-folders in this main folder. R locates the desired data by a command in line 41 that specifies where this data resides. In this example, whose file structure is illustrated to the left, we must modify line 41 to read: " excelpath="Habitat Data/"

Install the R Studio Program

If you have never used R or R Studio before, you will obviously need to download the programs to your computer. The job is relatively simple, but it is sometimes confusing. R, unlike many other software programs you may have installed, is an open source, collaborative program/project, and is supported by many Universities and other organizations across the country. You will choose a source from which you will download R and R Studio, and there are many (R asks you to select a CRAN source which is simply a location, like a University website, which supports the development and distribution of the program. Go online and search for Downloading R Studio, and pick one of the sources. I usually use the r-project.org for access to the R CRAN sources.

R Studio is a separate program that simplifies using R (the underlying code for your projects). It allows you to organize and print out the results of your run as a document in several different formats (I.e., a Word document). It also allows you to run the program in steps that helps ensure the program is running properly. If you require further assistance, there are many online sources to help you out.

Assuming you now have the R and R Studio programs installed, lets get started building your first FreshCervid run. Return to Slide 3 of this Tutorial to begin.

Click here to return to slide 3